

REMARKS

Upon entry of the foregoing amendments, claims 1–4, 10–14, 16, 18, 19, 25 and 26 are pending. Applicants have amended claims 3 and 4 to correct antecedent basis. Thus, claims 3 and 4 now recite “polynucleotides.” Basis for these amendments can be found in the specification as originally filed, and in particular, in originally filed claims 1 and 2. Applicants have amended claim 13 to correct improper dependency. Thus, claim 13 now recites “the host cell of claim 12.” Applicants have amended claim 19 to correct clerical errors and improper dependency. Thus, claim 19 now recites “the vaccine vector of claim 16.” Applicants have amended claim 25 to correct clerical errors. Applicants have added new claims 38 and 39 to more accurately claim the present invention. New claims 38 and 39 further limit the type of host cells to be used in the present invention. Specifically, new claims 38 and 39 are directed to mammalian cells and human cells respectively. Basis for these amendments can be found in the specification as originally filed, and in particular, at pg. 14, lines 9–14; pg. 15, line 31; and in originally filed claim 17.

These amendments add no new matter.

Co-Pending Applications

Applicants acknowledge the Examiner’s request regarding copies of claims, correlated with the serial number of the case in which they appear, for each pending application directed to the pending subject matter.

Applicants respectfully submit that acquiescing to the Examiner’s request of providing copies of pending claims would be unduly onerous and expensive for Applicants. Applicants have **no obligation to provide the Examiner with copies of claims in any pending applications**. In fact, Applicants submit that, under M.P.E.P. §804, it is the Examiner’s burden to identify any potential statutory and/or “obvious-type” double patenting rejections. *See*, M.P.E.P. §804(I)(B), which states:

Occasionally, the examiner becomes aware of two copending applications filed by the same inventive entity, or by different inventive entities having a common

inventor, and/or that are filed by a common assignee that would raise an issue of double patenting if one of the applications became a patent.

However, Applicants agree to provide the Examiner copies of the requested claims upon determination of allowable subject matter in the present application.

Drawings

Applicants acknowledge the Draftsperson's objection to the Drawings filed in the present application.

Applicants will provide formal drawings upon determination of allowable subject matter in the present application.

Oath/Declaration

Applicants acknowledge the Examiner's objection to the Declaration as filed in the present application. Applicants have enclosed herewith an executed Declaration. Accordingly, Applicants believe that the present objection is now moot.

Specification

The Examiner has objected to the Specification as having various informalities.

Applicants have amended the Specification to correct these informalities. Accordingly, Applicants believe that the present objection is now moot.

Provisional Double Patenting Rejection over Co-pending Applications

The Examiner has provisionally rejected claims 1–4, 10–14, 16–19, 25 and 26 under 35 U.S.C. §101 as claiming the same invention as that of claims 1, 20, 21, 25–28, 32–35, 41 and 42 of co-pending application U.S.S.N. 09/376,770 (“770”).

Applicants traverse. 37 CFR §1.78(b) provides that when two or more applications filed by the same Applicant contain conflicting claims, elimination of such claims from all but one application may be required in the absence of good and sufficient reason for their retention

during pendency in more than one application. However, the M.P.E.P. clearly states that “[t]his paragraph is appropriate only when the conflicting claims are **patentably distinct**. See MPEP §822. *See also*, In re Zickendraht, 319 F.2d 225, 138 USPQ 22 (CCPA 1963) (where the Court held that the doctrine is well established in that claims in different applications need be more than merely different in form or content and that **patentable distinction must exist to entitle applicants to a second patent**).

The ‘770 application is a co-pending application having the both the same inventive entity and assignee. However, both applications are directed to distinct sequences encoding *different Chlamydia* polypeptides. Applicants have attached herewith an alignment comparison between the polypeptide of the present application with those disclosed by U.S.S.N. 09/376,770 (Exhibits A and B). The comparisons clearly show that the polypeptides according to the present invention are **completely different** from those disclosed in the ‘770 application.

Accordingly, in light of the arguments above, Applicants respectfully request reconsideration and withdrawal of the present provisional double patenting rejection.

35 U.S.C. §112, First Paragraph Rejections

The Examiner has rejected claims 1–4, 10–14, 16–19, 25 and 26 under 35 U.S.C. §112, first paragraph as containing subject matter which was not described in the Specification in such a way as to enable one skilled in the art to make and/or use the invention, stating that the Specification is not enabled for a polynucleotide encoding a polypeptide having a sequence that is “at least 75% homologous” to SEQ ID NO:2 and “functional fragments thereof.” Specifically, the Examiner has alleged that:

Without a clear and unambiguous description of how to perform the comparison, the scope of the claims can not be envisaged (*sic*). Without a specific disclosure of the parametric values used in the algorithm, the sequence identity between two sequences has no common meaning within the art and therefore, one of ordinary skill in the art cannot be sure of the sequences embraced by the claims and would not be able to make and use those polynucleotide or polypeptide sequence homologs as recited in the instant claims, without undue experimentation.

See *e.g.*, December 13, 2000 Office action at pg. 5.

Applicants traverse. Methods and computational programs for conducting sequence comparisons for homology are well known within the art. Homology is typically measured using **sequence analysis software** (*e.g.*, Sequence Analysis Software Package of the Genetics Computer Group, University of Wisconsin Biotechnology Center, 1710 University Avenue, Madison, WI 53705). Similar amino acid sequences are aligned to obtain the maximum degree of homology (*i.e.*, identity). To this end, it may be necessary to artificially introduce gaps into the sequence. Once the optimal alignment has been set up, the degree of homology (*i.e.*, identity) is established by recording all of the positions in which the amino acids of both sequences are identical, relative to the total number of positions.

The Specification also describes a preferred method for determining amino acid similarities, including amino acid sequence homology:

One particularly preferred method of determining amino acid similarities is the PAM250 matrix described in Dayhoff *et al.*, 5 ATLAS OF PROTEIN SEQUENCE AND STRUCTURE 345-352 (1978 & Supp.), incorporated by reference herein. A similarity score is first calculated as the sum of the aligned pairwise amino acid similarity scores. Insertions and deletions are ignored for the purposes of percent homology and identity. Accordingly, gap penalties are not used in this calculation. The raw score is then normalized by dividing it by the geometric mean of the scores of the candidate compound and the reference sequence. The geometric mean is the square root of the product of these scores. The normalized raw score is the percent homology.

See *e.g.*, Specification at pg. 9, lines 15–23. Furthermore, the Specification specifically and clearly defines a "homologous amino acid sequence" as:

an amino acid sequence that differs from an amino acid sequence shown in SEQ ID NO: 2, only by one or more conservative amino acid substitutions, or by one or more non-conservative amino acid substitutions, deletions, or additions located at positions at which they do not destroy the specific antigenicity of the polypeptide. Preferably, such a sequence is at least 75%, more preferably 80%, and most preferably 90% identical to an amino acid sequence shown in SEQ ID NO: 2. Homologous amino acid sequences include sequences that are identical or substantially identical to an amino acid sequence as shown in SEQ ID NO: 2.

Id at pg. 8, lines 21–29. The Specification also describes amino acid sequence identity and conservative substitutions as:

By "amino acid sequence substantially identical" is meant a sequence that is at least 90%, preferably 95%, more preferably 97%, and most preferably 99% identical to an amino acid sequence of reference and that preferably differs from the sequence of reference, if at all, by a majority of conservative amino acid substitutions. Conservative amino acid substitutions typically include substitutions among amino acids of the same class. These classes include, for example, (a) amino acids having uncharged polar side chains, such as asparagine, glutamine, serine, threonine, and tyrosine; (b) amino acids having basic side chains, such as lysine, arginine, and histidine; (c) amino acids having acidic side chains, such as aspartic acid and glutamic acid; and (d) amino acids having nonpolar side chains, such as glycine, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan, and cysteine.

Id at pg. 9, lines 8–14. Thus, Applicants assert that one of ordinary skill in the art could make and use such homologous sequences in, for example, vaccines and diagnostic reagents.

Accordingly, Applicants respectfully request reconsideration and withdrawal of the present rejection.

35 U.S.C. §112, Second Paragraph Rejections

The Examiner has rejected claims 3, 4, 13, 17 and 19 under 35 U.S.C. §112, second paragraph, as being indefinite for improper antecedent basis.

Applicants have amended claims 3 and 4 to correct antecedent basis. Thus, claims 3 and 4 now recite "polynucleotides." Basis for these amendments can be found in the specification as originally filed, and in particular, in originally filed claims 1 and 2. Applicants have amended claim 13 to correct improper dependency. Thus, claim 13 now recites "the host cell of claim 12." Applicants have amended claim 19 to correct improper dependency. Thus, claim 19 now recites "the vaccine vector of claim 16." Applicants have added new claims 38 and 39 to more accurately claim the present invention. New claims 38 and 39 further limit the type of host cells to be used in the present invention. Specifically, new claims 38 and 39 are directed to mammalian cells and human cells respectively. Basis for these amendments can be found in the specification as originally filed, and in particular, at pg. 14, lines 9–14; pg. 15, line 31; and in originally filed claim 17.

In light of the above amendments, Applicants believe that the present rejections are now moot. Accordingly, Applicants respectfully request reconsideration and withdrawal of the present rejections.

35 U.S.C. §102 Rejection

The Examiner has rejected claims 1–4, 10–13, 16–19, 25 and 26 under 35 U.S.C. §102(b) as being anticipated by Longbottom *et al.* (**Longbottom**). Specifically, the Examiner has stated that **Longbottom** teaches “*chlamydial* genes or sequences coding for highly immunogenic protein fragments comprising 8 or 9 amino acid residues.”

Applicants traverse. **Anticipation requires the disclosure in a single prior art reference of each element of the claim under consideration.** *W.L. Gore & Associates v. Garlock, Inc.*, 220 USPQ 303, 313 (Fed. Cir. 1983), *cert. denied*, 469 U.S. 851 (1984); *Connell v. Sears Roebuck & Co.*, 220 USPQ 193, 198 (Fed. Cir. 1983); *Verdegai Bros. v. Union Oil Co. of California*, 2 USPQ2d 1051, 1053 (Fed. Cir. 1987); *In re Spada*, 15 USPQ2d 1655 (Fed. Cir. 1990); MPEP § 2131. “**There must be no difference between the claimed invention and the reference disclosure, as viewed by a person of ordinary skill in the field of the invention.**” *Scripps Clinic & Research Foundation v. Genentech Inc.*, 18 USPQ 2d 1001, 1010 (Fed. Cir. 1991).

Although both applications are directed to *Chlamydia* polypeptides, **Longbottom** discloses distinct sequences encoding ***different Chlamydia*** polypeptides. Applicants have attached herewith an alignment comparison between the polypeptides of the present application with those disclosed by **Longbottom** (Exhibit C1 to C4). Applicants have highlighted the regions that the Examiner has suggested would be identical between the present application and **Longbottom**. As can be seen by the highlighted regions, the rejection seems to be based upon that of identical fragments within the polynucleotides and/or polypeptides of the present invention, **not on the *entire* polynucleotide or polypeptide**. Furthermore, the comparisons clearly show that the polynucleotides and polypeptides according to the present invention are, in

Applicants: Murdin *et al.*
Serial No. 09/428,122

fact, **different** from those disclosed in **Longbottom**. Thus, Applicants assert that the present application is not anticipated by **Longbottom**.

Accordingly, in light of the arguments above, Applicants respectfully request reconsideration and withdrawal of the present rejection.

CONCLUSION

On the basis of the foregoing amendments and remarks, Applicants respectfully submit that the pending claims are in condition for allowance. If there are any questions regarding these amendments and remarks, the Examiner is encouraged to contact the undersigned at the telephone number provided below.

Respectfully submitted,



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VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Specification:

The paragraph beginning at line 6, pg. 8 was amended as follows:

-- [FIG. 1] FIG. 1A to 1I shows the nucleotide sequence (top sequence) and the deduced amino acid sequence (bottom sequence) of the full length 98 kDa putative outer membrane protein gene (SEQ ID NO: 1) and the processed sequence from *Chlamydia pneumoniae* (SEQ ID NO: 2). --

The paragraph beginning at line 9, pg. 8 was amended as follows:

-- [FIG. 2] FIG. 2A to 2H shows the restriction enzyme analysis of nucleotide sequence encoding the *C. pneumoniae* 98 kDa putative outer membrane protein gene. --

The paragraph beginning at line 13, pg. 16 was amended as follows:

A recombinant expression system can be selected from prokaryotic and eukaryotic hosts. Eukaryotic hosts include yeast cells (*e.g.*, *Saccharomyces cerevisiae* or *Pichia pastoris*), mammalian cells (*e.g.*, COS1, NIH3T3, or JEG3 cells), arthropods cells (*e.g.*, *Spodoptera frugiperda* (SF9) cells), and plant cells. Preferably, a prokaryotic host such as *E. coli* is used. Bacterial and eukaryotic cells are available from a number of different sources to those skilled in the art, *e.g.*, the American Type Culture Collection [(ATCC; Rockville, Maryland)] (ATCC; 10801 University Boulevard, Manassas, VA 20110-2209).

In the Claims:

3. (Amended) The polynucleotide of claim 2 wherein the fusion polypeptide is a heterologous signal peptide.

4. (Amended) The polynucleotide of claim 2 wherein the polynucleotide encodes a functional fragment of the polypeptide having the SEQ ID NO: 2.
13. (Amended) The host cell of claim 12[0], wherein said host cell is a prokaryotic cell.
19. (Amended) A pharmaceutical composition, comprising an immunologically effective amount of the vaccine vector of claim 16[4].
25. (Amended) A polynucleotide probe reagent capable of detecting the presence of *Chlamydia* in a biological material, comprising a polynucleotide that hybridizes to the polynucleotide of claim 1 under stringent conditions.
- 38. (New) The host cell of claim 14, wherein said eukaryotic cell is a mammalian cell.
39. (New) The host cell of claim 38, wherein said mammalian cell is a human cell.--

EXHIBIT C - The Alignment of LONGBOTTOM to CPN 100396 (SEQ ID NO:1)

Alignment 1

GAP of: cpu72499.seq check: 4475 from: 1 to: 4926

WPDEF Chlamydomophila abortus putative outer membrane protein gene, partial
LOCUS CPU72499 4926 bp DNA BCT 13-MAY-1999
DEFINITION Chlamydomophila abortus putative outer membrane protein gene, partial
cds; and putative 98 kDa outer membrane protein gene, complete cds.
ACCESSION U72499
VERSION U72499.1 GI:1657776 . . .

to: cpn100396.seq check: 452 from: 1 to: 3000

WPDEF
cpn100396

Symbol comparison table: /big1/gcg/gcgcore/data/rundata/nwsgapdna.cmp
CompCheck: 8760

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	0.000
Quality:	14521	Length:	5027
Ratio:	4.840	Gaps:	13
Percent Similarity:	53.087	Percent Identity:	53.087

Match display thresholds for the alignment(s):

| = IDENTITY
: = 5
. = 1

cpu72499.seq x cpn100396.seq March 2, 2001 11:29 ..

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1951 CAAGCAGTCCTCTCTAGAACGCAGGGGCCTCTTACCAAAAAATGACAAAAA 2000
      |
      1 .....cgctct 6
2001 CATGTCAAGTCCTTTCTGTATTAGACTTGCTTTCTTTGTATCTTTGAGT 2050
      | |      || ||      |||| || ||| | || | ||
      7 tacctagtagagggttgagtgaatttcttgactggttctcctattggtgt 56
2051 ATTTAACGAACTGTTTTTTTCATTTACCCACA.AGTGTATAAAATGAGG 2099
      || | ||| | || | ||| | || | ||| ||| |
      57 atctcttaaaatattaaattcaaaatcaaagtatatattttacaatgaag 106
2100 CCTTCTTTATATAAGATTTTAATATCGTCGACGCTGACGTTACCAATATC 2149
      ||||| ||| || || || | || | || || ||
      107 tcttctttccccaagtttgatctttctacatttgctattttccctttgtc 156
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2150 TTTTCACTTCTCGCAATTGCATGCAGAAGTGGCTTTAACTCAAGAATCTA 2199
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 157 tatgattgctac.....cgagacagttttggattcaagtgcgagtttcg 200
 2200 TTCTCGATGCAAATGGAGCATTTCAGTCCGCAATCTACAAGCACTGCGGGA 2249
 | | | | | | | | | | | | | | | | | |
 201 atgggaataaaaaatggtaatttttcagttcgtgagagtcaggaagatgct 250
 2250 GGAACGATTTACAACGTCGAGAGTGATATTTCTATTGTAGATGTAGGACA 2299
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 251 ggaactacctacctattttaagggaaatgtcactctagaaaatttcctgg 300
 2300 GACAG...CGGCTCTTGCTTCCTCAGCTTTTGTTCAGACTGCAGACAACC 2346
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 301 aacaggcacagcaatcacaaaaagctgttttaacaacactaagggcgatt 350
 2347 TAACTTTCAAAGGGAACAACCATAGCTTATCCATAACGAACGCGAATGCC 2396
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 351 tgactttcacaggtaacgggaactctctattgttccaaacggtggatgca 400
 2397 GGAGCTAATCC...TGCGGGAATTAACGTTAACTGCCCATAAGATTCT 2443
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 2444 TACGCTGACAGATTTTTCTAAGTTGAGCTTTAAGGAATGCCATCTTCTC 2493
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 2494 TAGTGAATACTGGAAAAGGGC...TATGAAATCCGAGGAGCATTAAC 2540
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 2541 TTAGCGAATAATGCCAGTATTCTGTTTGATCAGAACTATTCCGCTGAGAA 2590
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 2591 TGGTGGAGCCATCTCTTGCAAAGCTTTTTCTCTAACCGGCTCGAGCAAAG 2640
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 2691 GCTACGGGAATAGCTCATCTTTTCGGACAACCAAGGCACAATCAGATTTTC 2740
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851 ggagcgagctcctcaacaacgggggatatgtcaggaggtgctatctgtgc 900
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 901 ttataaaactagtacagatactaaggtcacctcactggaaatcagatgt 950
 2926 TGATTTTTGAGGAAAATACTTCTTCAGCAAAAGGTGGAGCGATTACACC 2975
 951 tactcttcagcaacaatacatcgacaacagcgggaggagctatctatgtg 1000
 2976 GATAAACTCATATTGACTTCTGGTGGGCCTACGGCATTATCAATAACAA 3025
 1001 aaaaagctcgaactggcttcgaggacttaccctattcagtagaaatag 1050
 3026 AGTTACCCATGCTACA...CCTAAGGGTGGAGCTATTGGTATTGCTGCCA 3072
 1051 tgtcaatggaggtacagctcctaaaggtggagccatagctatcgaagata 1100
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 1101 gtggggaattgagtttatccgccgatagtgggtgacattgtcttttaggg 1150
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 1248 ccatctacttctatgatcccataactacaggatcatccacaacagttaca 1297
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 1298 gatgtcttaaaagttaatgagactccggcagattctgcactacaatatac 1347
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3561 TTAGATGGGAAAAAATTCGCCGTAGTCGATGCCGTTGCTGCTGGGAAGAA 3610
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 | | | | | | | | | | | | | | | | | | | | | |
 2624 tgccaagatgcaacgtacaatctaactcttggttatactgtggatcttgt 2673
 4661 CCGTCATAATCCAAGCTGTATGACAGGATTGGCGATCAATGACGTTTCCT 4710
 | | | | | | | | | | | | | | | | | | | | | |
 2674 tcgtagtaaccccgactgtacgacaacactgcaatttagcggtagattcct 2723
 4711 GGTAAACCACAGCTACGAATCTTGCTAGACAAGCTTTCATAGTTCGCGCG 4760
 | | | | | | | | | | | | | | | | | | | | | |
 2724 ggaaaaccttcggtacgaatttggcaagacaagcttagtccttcgtgca 2773
 4761 GGTAACCATATTGCCTTAACCTCTGGTGTGAGATGTTGAGTCAGTTTGG 4810
 | | | | | | | | | | | | | | | | | | | | | |
 2774 gggaaccatttttgctttaactcaaattttgaagccttagccaattttc 2823
 4811 TTTCGAATTACGAAGCTCTTCAAGAAATTATAACGTAGATCTTGGCGCTA 4860
 | | | | | | | | | | | | | | | | | | | | | |
 2824 ttttgaattgcgtgggtcatctcgcaattacaatgtagacttaggagcaa 2873
 4861 AGGTCGCGTTCTAAAAAGCTCCCCCTGCCAGCTCTGGGCAGGGTTCTC 4910
 | | | | | | | | | | | | | | | | | | | | | |
 2874 aataccaattctaatacggttagcttttggtaaagagctccatacatcgaag 2923
 4911 CTTATTCTAGTCTAGA..... 4926
 | | | | | | | | | | | | | | | | | | | | | |
 2924 ggaaaagagcttttaagatttcttgaaggctcttttcgatttcgatttcc 2973

Alignment 2

GAP of: cpu65942.seq check: 1642 from: 1 to: 6110

WPDEF Chlamydomophila abortus strain S26/3 POMP91A and POMP90A precursor,
LOCUS CPU65942 6110 bp DNA BCT 07-MAY-1999
DEFINITION Chlamydomophila abortus strain S26/3 POMP91A and POMP90A precursor,
genes, complete cds.
ACCESSION U65942
VERSION U65942.1 GI:1617505 . . .

to: cpn100396.seq check: 452 from: 1 to: 3000

WPDEF
cpn100396

Symbol comparison table: /big1/gcg/gcgcore/data/rundata/nwsgapdna.cmp
CompCheck: 8760

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	0.000
Quality:	13146	Length:	6140
Ratio:	4.382	Gaps:	20
Percent Similarity:	49.428	Percent Identity:	49.428

Match display thresholds for the alignment(s):

| = IDENTITY
: = 5
. = 1

cpu65942.seq x cpn100396.seq March 2, 2001 13:39 ..

```
2251 CTTTAAGGAAAACAATAGCGATCAAGGAAGATACTTTGAAAAGTAATAACC 2300
      || || | | | | | | | |
1 .....cgctcttacctagtagaggttgagtgaatttctt 34

2301 TCACCAACTTATCTATGCCCATAGGTGTGAAATTGGAAAAATTCTCTCAC 2350
      | ||| | | | | | | | |
35 gacttgtttctcctattgggtgtatctcttaaaatattaaattcaaaatca 84

2351 AAGGATACCGCTTCTTACAACCTTACCCTGGCTTATGCTCCAGATATCGT 2400
      ||| ||| | | | | | | | | | |
85 aagtatatattttacaatgaagtcttctttccccaagtttgatattttcta 134

2401 AAGAAGCAACCCTGACTGTACTGCCTCTCTGTTAGTGAGCCCAACCTCTG 2450
      | || | | | | | | | | | |
135 catttgc.....tattttccctttgtctatgattgctaccgaga 173

2451 CTGTCTGGGTAACCTAAAGCTAATAACCTTGCGCGGCATGCTTTCATATTA 2500
      ||| ||| | | | | | | | | | |
174 cagtttttgattcaagtgcgagtttcgatgggaataaaaaatggtaatttt 223
```

2501 CAAGCAGGAAATTACTTGGCTTTAACTCGCAACACGGAGCTCTTCAGTCA 2550
 || | | | | | | | | | | | |
 224 tcagttcgtgagagtcaggaagatgctggaactacctacct....attta 269
 2551 ATTTCGGTTTCGAACTCCGAGGTTCTTGCCGCACCTATAACATAGATCTCG 2600
 | | | | | | | | | | | | | | | |
 270 agggaaatgtcactctagaaaatattcctggaacaggcacagcaatcaca 319
 2601 GATCGAAGATCCAGTTCTAATCTCATCCACCTCCCCTGCTCCGTAGACAC 2650
 | | | | | | | | | | | | | | | |
 320 aaaagctg.....ttttaacaacactaaggcgatttgactttcacag 362
 2651 GGAGCAGGGCCTCCCTTTGTCTACTCTAGCTGGTGACCTTGACTTTTAAAT 2700
 | | | | | | | | | | | | | | | |
 363 gtaacgggaactctctattgttccaaacggtggatgcagggactgtagca 412
 2701 TATTTTTATGATCGAGTTAGGATATCTCAAATCACCCAAAGCATGAATTT 2750
 | | | | | | | | | | | | | | | |
 413 ggggctgctgtt.....aacagcagcgt 435
 2751 ATGAAACATCCAGTCTACTGGTTCTTAATATCCTCGAGCCTATTTGCCTC 2800
 | | | | | | | | | | | | | | | |
 436 ggtagataaatctaccacgtttatagggttttcttcgctatcttttattg 485
 2801 GAATTCTTTGAGCTTCGCTAACGACGCTCAAACAGCCTTAACTCCCTCCG 2850
 | | | | | | | | | | | | | | | |
 486 cgtctcctggaagttcgataactaccggcaaaggagccgttagctgctct 535
 2851 ATAGCTATAATGGAAATGTGACCTCTGAGGAGTTCCAGGTAAAAGAAACT 2900
 | | | | | | | | | | | | | | | |
 536 acgggtagcttgagtttgaca.....aaaaatgtcagtttg 572
 2901 TCATCAGGAACAACGTATACTTGTGAAGGCAATGTGTGTATCTCCTTTGC 2950
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 573 tcttcagcaaaaactt....ttcaacggataatggcgggtgctatcaccgc 618
 2951 AGGGAAAGATTTCAGGTCTAAAGAAAAGTTGTTTCTCAGCTACTGATAACC 3000
 | | | | | | | | | | | | | | | |
 619 aaaaactctttcattaacagggactacaatgtcagctctgttttctgaaa 668
 3001 TTACCTTCCTAGGAAACGGGTATACCTTTTGCTTTGATAATATTACTACT 3050
 | | | | | | | | | | | | | | | |
 669 atacctcctcaaagaaaggcgagccattcagacttccgatgcccttacc 718
 3051 ACAGCTAGTAACCCCGGAGCCATTAATGTTCAAGGTCAAGGAAAAACCTT 3100
 | | | | | | | | | | | | | | | |
 719 attactggaaccaaggggaagtctctttttctgacaa..... 756
 3101 AGGCATCTCAGGATTTTCTTTATTTTCATGTGCTTATTGTCCTCCAGGCA 3150
 | | | | | | | | | | | | | | | |
 757tacttcttcggattctggagctgcaatttttacagaag 794
 3151 CAACTGGTTACGGAGCTATACAGACTAAAGGCAACACAACCTTTAAAAGAT 3200
 | | | | | | | | | | | | | | | |
 795 cctcggtgactatttctaataatgctaaaagtttcctttattgacaataag 844
 3201 AACTCTAGTCTTGTCTTCCATAAAAACTGCTCAACAGCAGAAGGTGGGGC 3250

845 gtcacaggagcgagctcctcaacaacgggggatatgtcaggaggtgctat 894
 3251 TATCCAGTGTAAGGAAGCAGTGATGCTGAATTAAAAATAGAAAATAATC 3300
 895 ctgtgcttataaaaactagtagataactaaggtcacccctcactggaaatc 944
 3301 AGAATCTGGTTTTCTCAGAAAACCTCTCCACTTCAAAGGCGGGGCTATT 3350
 945 agatgttactcttcagcaacaatacatcgacaacagcgggaggagctatc 994
 3351 TATGCTGATAAACTCACCATTGTCTCAGGTGGGCCTACATTATTTTCTAA 3400
 995 tatgtgaaaaagctcgaactggcttcgaggacttaccctattcagtag 1044
 3401 CAACTCTGTATCCAACGGTTCATCCCCTAAAGGCGGAGCTATTAGCATAA 3450
 1045 aaatagtgtcaatggaggtacagctcctaaggtggagccatagctatcg 1094
 3451 AAGATTCAAGTGGTGAATGTAGCCTAACCGCTGATCTCGGAGATATTACC 3500
 1095 aagat...agtgggaattgagtttatccgccgatagtgggtgacattgtc 1141
 3501 TTCGATGGGAACAAAATCATCAAAACTAGTGGTGGAAGTTCTACAGTAAC 3550
 1142 ttttagggaatacagtcacttctactactcctgg.....gacgaatag 1185
 3551 AAGAAATTCCATAGATCTCGGCACAGGGAATTTACAAAGCTACGTGCTA 3600
 1186 aagtagtatcgacttaggaacgagtgcaaagatgacagctttgcgttctg 1235
 3601 AAGACGGCTTCGGAATTTTCTTCTATGACCCTATTACTGGGGGAGGAT.. 3648
 1236 ctgctggtagagccatctacttctatgatcccataactacaggatcatcc 1285
 3649CTGATGAACTAAACATTAATAA.....AAAAGAAAC 3679
 1286 acaacagttacagatgtcttaaaagttaatgagactccggcagattctgc 1335
 3680 TGTTGATTATACAGGAAAGATCGTCTTCTCAGGTGAAAAATTATCCGATG 3729
 1336 actacaatatacaggggaacatcatcttcacaggagaaaagttatcagaga 1385
 3730 AAGAAAAAGCACGAGCGGAAAACCTAGCTTCTACTTTCAACCAACCCATC 3779
 1386 cagaggccgcagattctaaaaatcttacttcgaagctactacagcctgta 1435
 3780 ACATTATCAGCAGGATCTCTTGTACTTAAAGATGGTGTATCTGTAACCGC 3829
 1436 actctttcaggaggtactctatctttaaaacatggagtgactctgcagac 1485
 3830 AAAACAAGTAACGCAGGAAGCGGGATCTACCGTTGTCATGGATCTAGGGA 3879
 1486 tcaggcattcactcaacaggcagattctcgtctcgaaatggacgtaggaa 1535
 3880 CCACATTACAGACGCCTTCTTTCAGGTGGAGAAACCATCACCTAACTAAT 3929

1536 ctactctaga.....acctgctgatactagcaccataaacaat 1573

3930 CTAGATATTAACATCGCCTCGTTGGGGGGGGGGGGGGGTACCTCTCCTGC 3979
 || ||||| || | ||| ||

1574 ttggtcattaacatcagttctat.....agacggtgcaaagaaggc 1614

3980 TAAACTCGCAACAAATACAGCAAGTCAAGCTATAACTAT...TAACGCTG 4026
 ||| || ||| || | || ||| || |

1615 aaaaatagaaaccaaagctacgtcaaaaaatctgactttatctggaacca 1664

4027 TCAATCTAGTCGATGCTGATGGCAATGCTTATGAAGATCCTATTCT.... 4072
 ||| || || || | ||| ||||| ||| ||| ||

1665 tcactttattggacccgacgggcacgttttatgaaaatcatagtttaaga 1714

4073 ..TGCTACGTCTAAACCTTTACAGCAATAGTAGCTACAACCTAACGCTAG 4120
 || || ||| | || || | |||| | ||| |

1715 aatcctcagtcctacgacatcttagagctcaaagcttctggaactgtaac 1764

4121 TACAGTCACACAGCCTACAGATAATCTAACAAATTATGTCCCTCCTACTC 4170
 | | | | | | | | | | | | | | | |

1765 aagcaccgcagtgactccagatcctataatgggtga.....gaaattcc 1808

4171 ATTACGGTTACCAAGGAAATTGGACAGTAACCTGGGACACCGAAACAGCT 4220
 ||||| || || ||| ||| || | ||| |||

1809 attacggctatcaggaacttggggcccaattgtttgggggacaggggct 1858

4221 ACAAAAACAGCCACTCTAACTTGGGAACAACTGGCTACTCCCCTAACCC 4270
 | | || ||| || | ||| ||||| ||||| |||

1859 tctacgactgcaaccttcaactggactaaaactggctatattcctaattcc 1908

4271 AGAACGTCAAGGACCTTTAGTCCCGAATACTCTTTGGGGTGCATTCTCTG 4320
 || ||| || ||||| |||| | ||| ||||| |

1909 cgagcgatcggctcttagtcctaataagcttatggaatgcatttatag 1958

4321 ACCTCAGAGCTATACAAACTTAATGGATATTAGCGTCAATGGCGCTGAC 4370
 | ||| || || | |||| | | ||| ||| |

1959 atattagctctctccattatcttatggagactgcaaacgaagggttgag 2008

4371 TACCATAGAGGTTTTTGGGTATCCGGTCTAGCTAACTTCTTACACAAAAG 4420
 | || ||||| || || ||||| ||||| |||

2009 ggagaccgtgctttttgggtgtgctggattatctaactcttccataagga 2058

4421 TGGCTCTGATACTAAACGCAAGTTCCGTCACAATAGCGCCGGATACGCTT 4470
 || | || || ||| ||| ||| || ||| ||| |||

2059 tagtacaaaaacacgacgcgggtttcgccatttgagtggcggttatgtca 2108

4471 TAGGCGTCTACGCAAAAACCTCTCTGATGATATTTTCAGTGGGCTTTC 4520
 |||| | || | ||| ||| ||| ||| ||||| ||| ||

2109 taggaggaaacctacatacttgttcagataagattcttagtgctgcattt 2158

4521 TGCCAACTCTTCGGAAAGGACAAAGACTATTTAGTGTGCAAAAAACAACGC 4570
 || || ||||| ||| || | ||||| || || ||| ||| |||

2159 tgtcagctctttggaagagatagagactactttgtagctaagaatcaagg 2208

4571 CAACATTTACGCAGGTTCTCTCTATTATCAGCATATCTCCTATTGGAGCG 4620
 | || ||||| ||||| ||||| ||| ||| |||

2209 tacagtctacggaggaactctctattaccagcacaacgaaacctatatct 2258

4621 CTTGGCAGAATCTGCTACAAAACACTATCGGTGCAGAAGCTCCGTTAGTC 4670
 || | ||| | | | ||
 2259 ctcttccttgcaaactacggccttggtcgttgcttatgttcctacagag 2308
 4671 CTTAACGCACAGTTAACTTATTGTCATGCTTCAAACGACATGAAAACCAA 4720
 || | | || | | | | | | | | | | |
 2309 attcctgttctcttttcaggaaaccttagctacaccatacggataacga 2358
 4721 CATGACGACTACTTACGCTCCTCGTAAAACAACGTATGCAGAAATCAAGG 4770
 ||| || | | | | | | | | | | | |
 2359 tctgaaaaccaagt.....atacaacatatcctactgttaaag 2396
 4771 GTGATTGGGGTAACGATTGTTTCGGAGTCGAGCTTGGTGCAACTGTGCCT 4820
 | |||| | | ||| |||| | | | | | | | |
 2397 gaagctgggggaatgatagtttcgctttagaattcggtggaagagctccg 2446
 4821 ATCCAAACAGAATCTTCTCTCTATTCGATATGTACTCACCTTTCCTGAA 4870
 || ||| | |||| | | ||| | | ||| ||||
 2447 atttgcttagatgaaagtgtctatattgagcagtagcatgcccctcatgaa 2496
 4871 GTTTCAACTTGTGCATACGCACCAAGATGACTTTAAGGAAAACAATAGCG 4920
 || | | |||| | | | | | | | | | | | |
 2497 attgcagtttgtctatgcacatcaggaaggttttaagaacaggggaacag 2546
 4921 ATCAGGGAAGATACTTCGAAAGCAGCAATCTCACCAACCTTCTCTGCCT 4970
 | | | | | | | | | | | | | | | | | |
 2547 ...aagctcgtgaatttggaagtagccgtcttgatcctgccttacct 2593
 4971 ATCGGCATCAAGTTTGAGAGATTGCTAACAACGATACAGCTTCTTATCA 5020
 |||| | | |||| | | | | | | | | | |
 2594 atcgggatccgatttgataaggaatcagactgccaagatgcaacgtacaa 2643
 5021 TGTCCTGCTGCTTATTCTCCTGATATCGTAAGAAGTAACCCTGACTGTA 5070
 | | || | | |||| | | | | | | | | | | | |
 2644 tctaactcttggttatactgtggatcttggttcgtagtaaccccgactgta 2693
 5071 CTACTTCTCTGTTAGTAAGCCCCGACTCTGCTGTCTGGGTAACGAAAGCC 5120
 | | | | | | | | | | | | | | | | | |
 2694 cgacaacactgcaatttagcgggtgattct.....tggaaaaccttcggt 2737
 5121 AACCAACCTTGCGCGAAGCGCCTTCATGCTACAAGCAGGAACTACTTGTC 5170
 | | | | | | | | | | | | | | | | | |
 2738 acgaatttggcaagacaagcttttagtccttcgtgcagggaaaccatttttg 2787
 5171 TTAAAGTCACAACATAGAAATCTTCAGCCAGTTCGGTTTCGAGCTCAGGG 5220
 || | || | ||| ||| |||| | | ||| | | | |
 2788 ctttaactcaaattttgaagccttttagccaattttcttttgaattgcgtg 2837
 5221 GATCTTCACGAACCTATAACGTAGATCTCGGATCGAAGATCCAGTTCTAA 5270
 | | | | | | | | | | | | | | | | | |
 2838 ggtcatctcgcaattacaatgtagacttaggagcaaaataccaattctaa 2887
 5271 TCTCATCCACCTCTCCTACCCCGTTCCACGGGGTAGGGCCTTATAACCT 5320
 | | | | | | | | | | | | | | | | | |
 2888 t.gcgttagcttttggtaaagagctccatacatcgaagggaaaagagcttt 2936

Alignment 3

GAP of: pomp90.pep check: 1153 from: 1 to: 839

WPDEF prt
pomp90 prt

to: 396prt.pep check: 2118 from: 1 to: 928

WPDEF
396prt

Symbol comparison table: /big1/gcg/gcgcore/data/rundata/blosum62.cmp

CompCheck: 6430

BLOSUM62 amino acid substitution matrix.

Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid substitution matrices from protein blocks. Proc. Natl. Acad. Sci. USA 89: 10915-10919.

Gap Weight: 8 Average Match: 2.912
Length Weight: 2 Average Mismatch: -2.003

Quality: 1485 Length: 958
Ratio: 1.770 Gaps: 29
Percent Similarity: 54.512 Percent Identity: 47.960

Match display thresholds for the alignment(s):

| = IDENTITY
: = 2
. = 1

pomp90.pep x 396prt.pep March 2, 2001 16:59 ..

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1 MKHPVYWFLISSSLFASNSLSFANDAQTALTPSDSYNGNVTSEEFQVKET 50
  || . | . || | : | | | : | . | | : |
1 mkssfpkfvfst..faifplsmi.atetvldssasfdgn.kngnfsvres 46

51 ..SSGTTYTCEGNVCI.SFAGKDSGLKKSCFSAT.DNLTFLGNGYTLCFD 96
  . || | | . || | : . | . : || | | . | . || | || | . | |
47 qedagttylfkgnvtlenipgtgtaitkscfnntkgdltftgngnsllfq 96

97 NITTTASNPGAINVQGGKTLGISGFSLFSCAYCPPG..TTGYGAIQ.TK 143
  : . | : | . | . || | | | | | || | || : .
97 tvdagtvagaavnssvvdksttfigfsslsfiaspgssittgkgavscst 146

144 GNTTLKDNSSLVFHKNCST.....AEG 165
  | . . | | | | | | | |
147 gslsltknvsllfsknfstdnnggaitaktlsltgttmsalfsentsskkg 196

166 GAIQ..... 169
  || | |
197 gaiqtsdaltitgnqgevfsdntssdsgaaifteasvtisnnakvsfid 246

170 .....C..KGSSDAELKIENNQNLFSENSSTSKGG 198
  | | | . | . : || | . || | . || |
247 nkvtgasssttgdmssgaicayktstdtkvltgnqmlfsnntsttagg 296
```

```

199 AIYADKLTIVSGGPTLFSNNNSVSNSSSPKGGGAISIKDSSGECSLTADLGD 248
    ||| || : ||| |||| |||. ..||| |||. | ||| ||. || |
297 aiyvkklelasggltlfsrnsnvnggtapkggaiaied.sgelslsadsgd 345
    .
249 ITFDGNKIIKTSGGSSSTVTRNSIDLGT.GKFTKLRAKDGFGIFFYDPITG 297
    | | | | : |. |.. |. |||| | | | |. | | : |||| |
346 ivflgntvtsttpgtn...rssidlgtsakmtalrsaagraiyfydpitt 392
    .
298 GGS....DELNINK...KETVDYTGKIVFSGEKLSDEEKARAENLASTFN 340
    | | | | : |. . ||| | : |. |||| : | | .. || |
393 gssttvtldvlkvnetpadsalqytgniiftgeklseteaadsknltskll 442
    .
341 QPITLSAGSLVLKDGVSVTAKQVTQEAGSTVVM DLGTTLQTPSSGGETIT 390
    || : ||| |. | | | |.. . || : | |. | |. |||| : |. : | |
443 qpvtlsggtlslkhgvtlqtqaftqqadsrlemdvgttle.pa...dtst 488
    .
391 LTNLIDINIASLGGGGGTSPAKLATNTASQAITIN.AVNVLVDADGNAYEDP 439
    : || |||. | : | | | : | |. : | :. : |. | | |.
489 innlvinissi...dgakkakietkatsknltslsgtitlldptgtfyenh 535
    .
440 ILATSKPFTAI...VATTNASTVTQPTDNLTNYPPTHYGYQGNW.TVTW 485
    | . : : . | | | | | : : | | | | | | : |
536 slrnpqsydilelka sgvtvtstavtp.dpimg..ekfhgyggtwgpivw 582
    .
486 DTETATKTATLTWEQTYGSPNPERQGPLVPNTLWGAFSDLRAIQNLMDIS 535
    | . | || | |. ||| |||| | | ||||. || | | : :. || : .
583 gtgast.tatfnwtktygipnperigslvpnslnafidisslhylmeta 631
    .
536 VNGADYHRGFVWVSLANFLHKSGSDTKRKFRHNSAGYALGVYAKTPSDDI 585
    | | | | |. ||. || | |. | : | || | | | | : | | | |
632 neglqgdrafwcaglsnffhkdstktrrgfrhlsggyviggnlhctskdi 681
    .
586 FSAAFQCLFGKDKDYLVSKNNANIYAGSLYYQH....ISYWSAWQNLLQN 631
    ||||| : ||| |. || : | |. |||| | | | |
682 lsaafcqlfgrdrdyfvaknqgtvyggtlyyqhnetyislpcklrpsls 731
    .
632 TIGAEAPLVLNAQLTYCHASNMDKTNMTTTYAPRKTTYAEIKGDWGNDCF 681
    : | |.. . |. | | | : || : ||| : || | | | |
732 yvpteipvlfsnglsytthdndlkt.....kyttyptvksgwgn dsf 773
    .
682 GVELGATVPPIQTESSLLFDMYSPFLKFQLVHTHQDDFKENNSDQGRYFES 731
    . | | | | : | || : | || : | | : || : || | . : | | |
774 alefggrapicldesalfeqympfmklqfvyahqegfkeqgt.earefgs 822
    .
732 SNLTNLSLPIGIKFERFANNDTASYHVTAAYSPDIVRSNPDC TTSLLVSP 781
    | | ||. |||| : ||. . |. |.. |. | : |||| |||| |. : |
823 srlvnalalpigirfdkesdcqdatynltlgytvd | lrsn pdctt lrisg 872
    .
782 DSAVWVTKANNLARS AFMLQAGNYLSLSH NIEIFSQFGFELRGSSRTYNV 831
    || | | | | |. |. ||| : . | | | | | | | | | | |
873 ds..wktfgtnlarqalvlragnhfcfn snfeafsqfsfelrgssrnynv 920
    .
832 DLGSKIQF 839
    |||. | ||
921 dlgakyyqf 928

```

Alignment 4

GAP of: pomp91.pep check: 2232 from: 1 to: 847

WPDEF prt
pomp91 prt

to: 396prt.pep check: 2118 from: 1 to: 928

WPDEF
396prt

Symbol comparison table: /big1/gcg/gcgcore/data/rundata/blosum62.cmp

CompCheck: 6430

BLOSUM62 amino acid substitution matrix.

Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid substitution matrices from protein blocks. Proc. Natl. Acad. Sci. USA 89: 10915-10919.

Gap Weight: 8 Average Match: 2.912
Length Weight: 2 Average Mismatch: -2.003

Quality: 1468 Length: 967
Ratio: 1.733 Gaps: 29
Percent Similarity: 51.238 Percent Identity: 44.059

Match display thresholds for the alignment(s):

| = IDENTITY
: = 2
. = 1

pomp91.pep x 396prt.pep March 2, 2001 17:01 ...

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1 .....MKHPVYWFLISS 12
51 gttylfkgnvtlenipgtgtaitkscfnntkgdlftgngnsllfqtvda 100
13 SLIVSNSLYSEEPDQKTLTSAHSYNGNTNSEPFNPLSTSNNGTIYTCTG 62
: .. | | . | . . . | . : | |
101 gtvagaavnssvdksttfigfs.slsfiaspgssitt..gkgavscstg 147
63 NICIAYAGLDGSGLSSTCF.TD....TAGNLSFLGNGYTLCFDNITTQS 106
.: : . | | | | | | | | | . | | |
148 slslt...knvslfknfstdnnggaitaktlsltgttmsalfse.ntss 193
107 SHPGAISVSGTNKTLDISGFSLFSCAYCPPGATGYG.AIKAVGNTTIKDN 155
| | | | . | | . . : . . | | . | | . |
194 kkggaiq...tsdaltitg.nqgevsfsdntssdsgaafteasvtisnn 239
156 SSLVFHKNCSTG.....EGGAIQCKASSSEAEELKIENNQNQLVFAEN 196
. . | | | | | | | . | . : . : | | | . |
240 akvsfidnkvtgasssttgdmmsggaicayktstdtkvtltgnqmllfsnn 289

```

197 SSSSSGGAIYADKLTIVSGGPTLFSNNSVS.ASSPKGGAICIKDSGGECS 245
|. | | | : | | | | | | | . . . | | | | | | | | |
290 tsttaggaiyvkklelasggltlfsrnsvnggtapkggaiaieds.gels 338
246 LTADLGDITFDGNKIIKTNGGSPTVTRNSIDLGS SGKFTKLNAKEGFGIF 295
|. | | | | | | | : | . | . | | | | | . | | | | . | | :
339 lsadsgdivflgntvtst...tpgtnrssidlgtsakmtalrsaagraiy 385
296 FYDPITGGGS....DELNINK...QDTVDTGKIVFSGERLSDEEKKVAA 338
| | | | | | | | | : | | | | | : | | | : | | : |
386 fydpittgsstvtvdlkvnetpadsalqytgniiftgeklseteaadsk 435
339 NLKSDFKQPLKIGSGSLILKDGVTLETQSFTQTEGATVMDLGTTLQTPS 388
| | | | | . : | . | | | | | : | . . . | | . | | | : | .
436 nltskllqpvtlsggtlskhgvtlqtqftqqadsrlemdvgttle.pa 484
389 SGGETITLTNLDINVASLGGGGVAPDPAKVEATTESKVTIN.AVNLVDD 437
: | | : | | | : | | : | | | . | : . : | . |
485 ...dtstinnlvinnissidga...kkakietkatsknltlsgtitlldp 527
438 NGNAYEYPILAASQPFTAIEVRSGSSGSITKPTTNLENYT.PPTHYGYQG 486
| | | | | : : : | . : . | . : | : | | | | |
528 tgtfyenhslrnpqsydilelk..asgtvtstavtpdpimgfekfhygyqg 575
487 NW.TVTWKQGSSAQEKTATLTWEQTGYSPNPERQGS LVPNTLWGSFSDIR 535
| : | | . | | | | | . | | | | | | | | | | . | | |
576 twgpivwgtgast...tatfnwtktyipnperigslvpnslnwnafidis 622
536 AIQNLMDISVNGADYHRGFVWSGLGNFLHKSGSDTKRKFRHNSAGYALGV 585
. : | | : . | | | . | | | | | . | : | | | | | | : |
623 slhylmetaneglqgdrafwcaglsnffhkdstktrrgfrhlsggyvigg 672
586 YAQTPSEDVFSAAFCOLFGKDKDYLVSKNSSTVYAGSIYYQHISYWNTWN 635
| | : : | | | | : | | | | | | | | | | : .
673 nlhtcsdkilsaaafcolfgdrdrdyfvaknqgtvyggtlyyqhnetyisl 722
636 TLLQ....NTLGAEAPLVNLNAQLAYCHASNMMKTNMTDTYAPPKTTYSEI 681
|. . . . | | . . | . | | | . : | | | | | | | :
723 cklrpsclsyvpteipvlfsnglsythtdndlktk....y....ttyptv 764
682 KGDWGNDCFGVEFGAKAPI.ETASLLFDMYSPFVKLQLVHAHQDDFKENN 730
| | | | | | . | | : | | | | | | : | | | | | : | | |
765 kgswnndsfafeqgrapicldesalfeqympfmlqlqvahqegfkeqg 814
731 SDQGRYFESNNLTNLSMPIGVKLEKFSHKDTASYNLTLAYAPDIVRSNPD 780
. : | | | . | | | : | | | : : | | | | | | | : | | | |
815 t.earefgssrlvnlalpigrfdkesdcqdatynltlgytvdlvrsnpd 863
781 CTASLLVSPTS AVWVTKANNLARHAFILQAGNYLALTRNTELF SQFGFEL 830
| | . | : | | | | | | | : | . | | : | | | | | | |
864 ctttlrisgds..wktfgtnlarqalvragnhfcfnfnfeafsqfsfel 911
831 RGSCRTYNIDLGSKIQF 847
| | | | | | : | | | | | | |
912 rgssrnynvdlgakyqf 928